Method: To find out the published series three national databases (Ulakbim Turkish Medical Literature database, http://www.turkishmedline.com, http://medline.pleksus.com.tr) and two international databases (Pubmed and Science Citation Index (SCI)) were searched. Keywords for national databases were ["idrar yolu infeksiyonu" or "idrar yolu enfeksiyonu" or "urinary tract infection" or "üriner sistem infeksiyonu" or "üriner sistem enfeksiyonu"]. Keywords for Index Medicus and SCI-expanded were ["urinary tract infection" and Turkey]. Articles i)published before 1997 ii)resistance data of outpatient and inpatient strains were not analysed seperately iii)antibiotic susceptibility data were not given, were excluded. All studies used Kirby-Bauer disc diffusion test by using NCCLS/CLSI criteria for determination of antimicrobial resistance. Resistance data of inpatient and outpatient strains were compared by Chi-square test. A p value less than 0.05 was considered significant.

Results: Data for 25577 E.coli strains were obtained from 53 articles (28 articles from 1997—2001 period, 25 from 2002—2007 period). Of these starins 18106 were isolated from outpatients whereas 7471 from inpatients. The resistance rates and comparisons of 1997—2001 and 2002—2007 periods are shown in Table 1.

Conclusions: Trimethoprim sulphametoxazole resistance is very high and it cannot be recommended in the empirical treatment any more. Nitrofurantoin may be a cheap and reasonable option in uncomplicated UTI. Aminoglycosides and third-generation cephalosporins may be good choices in the treatment of complicated UTI. Carbapenems may be conserved for extended-spectrum beta lactamase producing strains. ESBL rate in the outpatient strains is alarming. Policies to constrain resistance such as antibiotic stewardship or restriction programmes should be implemented immediately.

doi:10.1016/j.ijid.2008.05.282

17.017

OXA- and MBL-Type Enzymes Among Uncommonly Isolated *Acinetobacter* Spp. in Asia-Pacific Nations: Natural Reservoir for Resistance Determinants

R. Mendes[1,*], J. Bell[2], J. Turnidge[2], M. Castanheira[1], R. Jones[1]

[1] *JMI Laboratories, North Liberty, IA, USA*
[2] *Women's and Children's Hospital, Adelaide, Australia*

Background: Acinetobacters (AC) other than *A. baumannii* (ACOB) are occasionally recovered from clinical sources, but OXA and MBL genes have rarely been reported. The aim of this study was to identify and characterize OXA and MBL genes in AC. Gene context of bla_{OXA-23} detected in *A. radioresistans* (AR) was also evaluated.

Methods: AC recovered from patients in 10 countries in the Asia-Pacific (APAC) region were tested by broth microdilution. Isolates with imipenem or meropenem MIC $\geq$8 mg/L were screened for MBL- (IMP-like, VIM-like, SIM-1, GIM-1, SPM-1) and OXA- (OXA-23, -24, -58 clusters) genes. OXA genes and surrounding sequences were assessed by PCR mosomal and plasmid DNA were performed. RNA extraction followed by reverse transcriptase-PCR was performed to access expression of bla_{OXA-23}. Species identification was confirmed by 16S rRNA.

Results: Among 543 AC isolates, 28.2% carried OXA (98.7%) or MBL (1.3%) genes, from which 2.6% were found ACOB. An *A. junii* (AJ) with bla_{OXA-23} and an AR with bla_{OXA-23} and bla_{OXA-58} were detected in 2 Indian centers, while an *A. johnsonnii* with bla_{IMP-4} and *A. calcoaceticus* (ACA) with bla_{OXA-58} were identified in the Philippines and China, respectively. IS*Aba1* and IS*Aba3* surrounded bla_{OXA-23} from AJ and bla_{OXA-58} from AR and ACA, respectively. The AR showed a putative O-sialoglycoprotein endopeptidase-encoding gene upstream of bla_{OXA-23}; gene expression was not detected; and bla_{OXA-23} and bla_{OXA-58} were located on the chromosome and plasmid, respectively. Susceptibility to polymyxin and tigecycline ($\leq$2 mg/L; no breakpoint criteria) was $\geq$98.9%.

Conclusion: High dissemination of OXA genes was detected, emphasizing their ability to spread among AC. The data suggest AR may be a natural reservoir for bla_{OXA-23}. bla_{IMP-4} has been previously detected in Hong Kong, Australia and now Philippines, highlighting spread in APAC.

doi:10.1016/j.ijid.2008.05.283

17.018

Mutation in DNA Gyrase and Topoisomerase IV of *V. cholerae* Causing Diminished Susceptibility to Ciprofloxacin

S. Ahmed[1,*], W.A. Khan[1], D. Saha[2], M.A. Salam[1], M.L. Bennish[3], M. Rahman[4]

[1] *International Centre for Diarrheal Disease Research, Bangladesh (ICDDR, B), Dhaka, Bangladesh*
[2] *Medical Research Council(UK), Basse, Gambia*
[3] *Mpilonhle, Mtubatuba, South Africa*
[4] *Family Health International, Bangkok, Thailand*

Background: Diminishing clinical response to ciprofloxacin (CIP) therapy at ICDDR, B correlated with decreased minimum inhibitory concentration (MIC) of *V. cholerae* to CIP, though strains remained susceptible using standard thresholds. To determine the cause of the diminished susceptibility, we investigated mutations in the quinolone-resistance-determining-region/analogous region of genes *gyr*A/B and *par*C/E that encode, respectively, quinolone targets DNA gyrase and topoisomerase IV.

Method: We studied 30 clinical isolates of *V. cholerae* O1 and 10 of *V. cholerae* O139 isolated during 1993—2006. Susceptibility was determined by standard disk diffusion (DD) and E-test methods and interpreted according to CLSI and manufacturer's instruction respectively. We extracted chromosomal DNA, amplified and sequenced the gene fragments and then edited, matched and aligned the sequences using suitable methods and software to identify mutations.

Results: No mutation was detected in 9 strains having a CIP MIC of 0.002—0.003 and a NA MIC of 0.125—0.5 μg/ml; a substitution (Asparticacid87Asparagine) was noted in *gyr*A was noted in 2 strains with a CIP MIC of 0.008—0.012 and a NA MIC of 4—8 μg/ml; a unique *gyr*A mutation in